AMENDMENTS TO THE CLAIMS

Claims 1-27 (canceled)

Claim 28 (currently amended) A method for detecting a target nucleotide sequence, and providing a partial helical enclosure of the target sequence, comprising the steps of:

(a) rendering the target nucleotide sequence substantially single-stranded;

(b) hybridizing the single-stranded target nucleotide sequence with a nucleic acid probe unit, comprising:

two overlapping oligonucleotide subunits which are joined together to form a linear probe unit prior to target hybridization, wherein the first oligonucleotide comprises three segments sequentially: a first probe linker on one end that hybridizes to a reporter linker of a reporter but does not bind the single-stranded target nucleotide sequence, a central sequence complementary to the single-stranded target nucleotide sequence, and an overlap linker on the other end; wherein the second oligonucleotide comprises two segments sequentially: a matching overlap linker that is hybridized to the overlap linker of the first oligonucleotide, and a second probe linker which hybridizes to a reporter linker of a reporter but does not bind the single-stranded target nucleotide sequence, said two part probe structure thereby creates a linear overlap between the probe and the reporter linkers;

(c) washing to remove any unbound probe;

(d) hybridizing reporters to the two probe linkers; and

(e) detecting the presence of reporters to indicate the presence of the target nucleotide sequence.

Claim 29 (canceled)

Claim 30 (previously presented) The method of claim 28, wherein the reporter comprises a labeled, double stranded polynucleotide sequence linked on one or both ends to a reporter linker.

Claim 31 (previously presented) The method of claim 30, wherein the double-stranded polynucleotide sequence is at least 100 bases long.

Claim 32 (previously presented) The method of claim 30, wherein two or more reporters form a reporter array by linking end-to-end via complementary reporter linkers.

Claim 33 (previously presented) The method of claim 32, wherein the length of the reporter array is determined by a ratio of terminator oligonucleotide to reporters, said terminator oligonucleotide terminates the reporter array by hybridizing to said reporter linker at the end of the reporter array.

Claim 34 (previously presented) The method of claim 32, wherein the reporter array comprises successive layers of type I and type II reporters, each of the type I and type II reporter comprises a first and a second reporter linker, wherein the first and the second reporter linker of a type I reporter is hybridized respectively to the second reporter linker of a type II reporter and to the first reporter linker of another type II reporter, except the first reporter linker of the type I reporter in the first layer of reporter is hybridized to a probe linker of a probe.

Claim 35 (previously presented) The method of claim 28, wherein a multi-linking unit is interposed between the reporter and the probe linker, said multi-linking unit comprises (i) a sequence that hybridizes to the probe linker and (ii) two or more sequences that hybridize to said reporter linker of the reporter.

Claims 36-58 (canceled)

Claim 59 (previously presented) The method of claim 28, wherein the overlap linker and or the probe linker comprises one or more TA sequence to facilitate interstrand crosslinking between complementary linkers during probe fabrication or use.

Claim 60 (previously presented) The method of claim 30, wherein said reporter linker further comprises a carbon spacer segment.

Claim 61 (previously presented) The method of claim 30, wherein the reporter linker sequence consists of SEQ ID NO. 76.

Claim 62 (withdrawn) The method of claim 34, wherein the proximal and distal linkers of the Type 1 reporter comprise SEQ I.D. NO. 86 and 87 and wherein the proximal and distal linkers of the Type II reporter comprise SEQ I.D. NO. 90 and 92, and where the dual reporter linkers of the composite probe unit comprise SEQ I.D. NO. 92.